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Anderson et al.

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In the Claims:

1. (amended) A high-throughput method for determining a biochemical function of a protein or polypeptide domain of unknown three dimensional structure and function comprising:

(A) identifying a putative polypeptide domain that properly folds into a stable polypeptide domain[, said stable polypeptide having a defined three dimensional structure];

(B) determining three dimensional structure of the stable polypeptide domain;

(C) comparing the determined three dimensional structure of the stable polypeptide domain to known three-dimensional structures in a protein data bank, wherein said comparison identifies known structures within said protein data bank that are homologous to the determined three dimensional structure; and

(D) correlating a biochemical function corresponding to the identified homologous structure to a biochemical function for the stable polypeptide domain.

In claim 11, please delete the term "PDB" and insert --protein data bank--.